

FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATC**ATG**CTTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTTGTCTGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGC
CACCGGGCCCTCCTGGCATTCAGGAAACCATGGAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCCTCGAGGGGAGCGGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCGGGGATTCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGGAACTTCTTTGATGTCATGACTGGTAGATTGGGGCCCCAGTATCAGG
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGATGTGTACC
TTATGCACAAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGCAAAATCAGAT
ACATCCAGCAATCATGCTGTCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGGACCAACGCTTCTCCACCTTTGCAGGATTCTGCTCTTTG
AAACTAAG**TAA**ATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTACATGTCTGTATTCAAAAAATTATT
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTGAGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATACTCAGCATCTTTATCAC
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTCTAT
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACAGTTTTTCAGG
AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCATTATTAGCTAATTTAGTGCCCTCCG
TGTTGAGCTTAGCCTTTGACCTTTCCCTTTTGATCCACAAAATACATTAAACTCTGAATTC
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT
AGAGAAAGATTTTGACCTGGCTTTAGATAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
ATGGAATAAACACACCTTTGTTAAAGATAAAAAAAA

FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686
><subunit 1 of 1, 246 aa, 1 stop
><MW: 26994, pI: 6.43, NX(S/T): 0
MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKDGKDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFFSSVETNIGNFFDVMGTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGFLLFETK
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Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGCATGGCAAGCTTGGGACCTCTGCTGGCCCTTGCCCT
GGCCCTGGCCAGCCAGCCTCTGCCCGCCGGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTT
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGC
AGGGGAGTAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACC
CCACCACCAACAAGTCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT
GGCCGGGCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCTGAAGTACATGA
CCAAAGTGGATCCAGGAGCGGGGCTGCAGGACCGCTGAACGTCATTATTTTCTCGGATCAC
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGCTGTTGTGAGCCTTTGGCCGGCCCTGGGAAAC
ACTCTGAGATATATAACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAGCC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC
ATCTTCTGGCCTTCGGACCTGATTTCAAATCCAATTCTAGAGCTGCTCCTATCAGTTCGGT
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCGCTGCCCAACAACGGATCCT
GGTCCAGGTTGATGTGCATGCTGAAGGGCCGCGCGGCACCTGCCCGCCTGTCTGGCCAGC
CACTGTGCCCTGGCACTGATTCTTCTCTCTGCTTGCATAACTGATCATATTGCTTGCTC
AGAAAAAACACCATCAGCAAAGTGGGCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA
ATAATAGCTTCATTAAACAATCAAGACCATGCACATTGTAAATACATTATTCTTGATAAT
TCTATACATAAAAGTTCCTACTTGTATAA

FIGURE 4

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDY
LTPDFPSLSYPNYTLMTGRHCEVHQMIGNYMWDPTTNKSF DIGV NKDSL MPLW WNGSEPLW
VTLTAKARKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASQQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIFSDHGMTDIFW
MDKVIELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFVSPLTLVADEGWFTENREMLPFWMNSTGRREGWQRGWHGYDNE LMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC**ATG**ACGCTCCTCC
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCGCTGGCCCACCATGACCCCTCCTCAGG
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCA
GGCCCCCCCCACCTGCTGGCTCGAGGTGCCAAGTGGGGGAGGCTTTGCCTGTAGCCCTGG
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCGGTGCTGCGGCCGAGGAGGTGTTGGAGGCAGACACCACCAGCGCTCCATCTCAC
CTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG
CGGTGCTCCAGAGCCTGCTGGTGCTGCGCCGCGGCCCTGCTCCCGCGACGGCTCGGGGCT
CCCCACACTGGGGCCTTTGCCTTCCACACCGAGTTCATCCAGTCCCCGTGCGCTGCACCT
GCGTGCTGCCCCGTTCACTG**TGAC**CCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGC
TCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATATGCCTCCCCCAACACT
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCTTACCCTA
TCACTGGCCTCAGGCCCCGAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT
TAAACAATTATTTAAGTGACGTGTATTATTAAACTGATGAACACATCCCCAAAA

FIGURE 6

MTLLPGLLFLTWLHTCLAHHDP SLRGHPHSHGTPHCYSAEELPLGQAPP HLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKL
AFAECLRCGCIDARTGRETAALNSVRL LQSLVLVLR RRPCSRDGSGLPTPGAF AFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAAC**ATG**CAGCTCGGCACTGGGCTCCTG
CTGGCCGCCGTCTTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTACCAAGTGCAC
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA
CTGCCACCCGGGTCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCTACGTATCCATCGCTTGCTGCCAGAC
CAGCCTCTGCAACCATGAC**TGA**CGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCAC
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCCACC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCCTAGGGAAGTCTGCGTGGAGTC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCTTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGC SHGSRCLRDSTHCVT TATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCCTCTAGGACATACACGGGACCCCTT
AACTTCAGTCTCCCCAAACCGCGCACCTCGAAGTCTTGAACCTCCAGCCCCGCACATCCACGCG
CGGCACAGGCGCGGCAGCGCGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG
CTGGGCTCGGGCGGGGAGTAGGGCCCGCGCAGGAGGCGAGGCTGTCATATTTCAGAGTC
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGCATGAGCCGCGGTGCTCTCGTGTCTGCTGGCGCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCGCGCGCGTGGTTCAGCGGCCAAAAGGTGTGTTTGTCTGACTTCAAGCATCCCTGCTA
CAAAATGCGCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCTTGCTT
GTGAGAGTGAGGGAGGAGTCTCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG
GCTTTGGAGGAATGGAGATGGGCAAACTCTGGTGCTGCCAGATCTCTACCAAGTGGTCTG
ATGGAAGCAATTCCAGTACCGAACTGGTACACAGATGAACCTTCTCGCGGAAGTGAAAG
TGTTGTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA
TGGAATGATGACAGGTGTAACATGAAGCACATTTATTTGCAAGTATGAACACAGAGATTA
ATCCAACAGCCCCGTGTAGAAAAGCCTTATCTTACAAATCAACAGGAGACACCCATCAGAAT
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA
AAGGAAGAACAACCACTAGTCCAAACCACTGCTACACTGTGGATTTCAAAGAGTACCAGAAA
GAAAGTGGCATGGAAGTATAATACTCATTGACTTGGTTCCAGAATTTTGTAACTCTGGATC
TGTTAAGGAATGGCATCAGAACATAGCTTGAATGGCTTGAATCACAAGGATCTGCACAA
GATGAACCTGTAAGCTCCCCCTTGAGGCAATATTAAAGTAATTTTATATGCTATATTATTC
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC
CCAAACTTCAAACCTTCAAGCAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC
GGGAGTATGTGTGTAGAGCAATTCCTTTTATTTCTTCCACCTTTCATAAGTTGTTATCTA
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA
GTGTTTGATAAAAAATGAACGTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT
GCTCTTTTGATTAAGAACTTATTACTGTTGCAACTGAATTCACACACACACAAATATAG
TACCATAGAAAAAGTTTGTCTCGAAATAATTCATCTTTCAGCTTCTCGCTTTTGTGCA
ATGCTAGGAAATCTCTCAGAAATAAGAGCTATTTCATTAAAGTGTATATAAACCTCCTC
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TTATTTTATAGCTTAAAATTAACAGATTTTGTAAATATGTAACCTTGTAAATAGGTGCATAA
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CAGGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTCTGAAATCAATGTGGTCCCTCTC
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AAAGTGTGCTCAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG
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ATTTTAGAAGGAAGGAACTACGAAATCGTGTGAAATGGGTTGGAACCCATCAGTGATTCG
CATATTCATTGATGAGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGCTCTTATCTCC
TAGTTTCTTCAATGCTTACGCTTGTCTTCTCAAGAGAAAGTTGTAACCTCTCTGCTCTTCA
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FIGURE 10

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230
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><MW: 30431, pI: 6.79, NX(S/T): 3
MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACE
SEGGVLLSLENAEQKLIESMLQNLTKPGTGISDGDWIGLWRNGDGQTSACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNKYCKYEPEINP
TAPVEKPYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSOG
RTKTSPNQSTLWISKSTRKESGMEV
```

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGAAATGAGAGAGCAGTGGAGTGGAGTCCGGGGTCTGGTTCGGGGTGGTCTGTCTGCTCTGGCATGCCCTG
CCACAGCCACTGGGGCCGAAGTGTCTCAGCCTCAAGTAGACACCACTGGGTCTGTCGAGGCGGGCAGGTGG
CGGTGAAGGGCAGACAGCCCTTGTGAATGTCTTTCTGGGCATTCCATTTCGCCAGCCGCCACTGGGGCTGACC
GGTTCCTCAGCCCAACACCCAGCAGCAGCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGGCTAC
AAGACGTGGAGAGCATGAACACAGCAGATTTGTCTCTCAACGGAAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCTTGCTCTCAAGCTCTATAGCCAGCTGAGTCCCCCGAGGGTCCGTAGGCGCGTCAAGTATGGTCTCATG
GAGGCGCTCTGATAACTGGCGCTGCCACTCTCATGATGGATCAGCTCTGGCTGCCATGGGAGTGTGGTCTGG
TTACACTCCAGTACGGCCTTGGGGTCTCTGGCTTCTCAGCATTGGAGATGAGCATGCACCTGGCAACCAAGGGT
TCTAGATGTCTGCTAGCTGCTTTGGCCTGGTGCAGAAACATCGCCCCCTTCGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGGCCGTGGGAGCATCATCTCTGGCTGGTCTGCTGCCAGTCTGACAGCTGGCTGTTCC
ACAGAGCCATCACACAGAGTGGGTTCATCACCACCCAGGGATCATCGACTCTCACCTTGGCCCTTAGCTCAGA
AATTCGCAAAACACTTGGCTCGAGCTCCAGCTCCCCGCTGAGATGGTGCAGTGCCCTTCAGCAAGAAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAATACTATCTCTCTCACCGTGTATGGCACTGTCTCCCCAA
GCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGTGTCAACAACCATGATTC
GCTGGCTCATCCCCAGGGGCTGGGGTCTCTCGATACAAATGGAGCAGATGAGCGGGAGGACATGCTGGCATCT
CAACACCGCTCTTGACCACTCTGGATGTGCCCTCAGATGATGCCACCGTCATAGATGAATCCTAGGAAGCA
ACTCGGACGCACAGCAATGCCAGGCTTCAGGAGATTCTAGGGTGACGTATTCATCAATGTTCCCACTGCA
GTTTTCAAGATCTGCTCGAGATTCTGGAAGCCCTGTCTTTCTATGATGTCAGCATCAGCCACCTCTTTTG
CGAAGATCAAACTGCTGGGTGAAGGCTGATCATGGGCGGAGGGTCTTTGTGTTCCGAGGTGCTCTTCTCA
TGGACAGAGCTCCCGCTGGCTTCTCAGAGGCCACAGAGGAGGAGAGAGCAGTAACTCAGCTGATGGGCC
AGTGGACCACTTTGGCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCTGGGCCCAATTCAACAGGCGG
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AGACGCTCCCCAGCAAGATACAACAGTGGCAACAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTTGAAGCC
AGGCTGAACCTTCTGGCTGGGCGAAACCACTCTCAAGTGTGGCAGAGTCCACGACGCGACCGCCCTCTC
CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGTCTGTGATGCGAGTTATGCTCTTTTGA
ATGTCAGAGGCGCCCTCCACCTCTGGGCGATGTACAAGTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT
CTTGCTGTAGGTTCTAGACATCTCTAGCTTCTGAGGACTCACTCCCCAGGAAGCTTCCCTGCCTTCTC
TGGCTGTGCGGCCCGAGTCTGCTCATTAGAGCACAGTCCACCGAGGCTAGCACCGTGTCTGTGTCTGTCT
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CCTGGAGCTAGGGGTTGTTGCTGAGTGAAGTGAACACAGAAATGGGAATGGCAGTCTGTAACCTGAAC
CCAGAGCTTCAAGTGGCCAAAGCCATCTCAGGCCCCACAGCAATTGTCCACTCGGCCAGAGGCTGATGCC
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TAAGCCCTCAGACTAGGGCGGGAGGGTCTCTCTCTCTGCTGCCAGTCTGGGCCCTGCAACAAGACACAGA
ATCATCAGGGCCATGAGTGTCAACCAAGCTGACCTCAACAAATCCAGCCCTGACCTCAGGACGCTGGAT
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AGCACCCACAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACAGGGCATCCGTGGGCTATTGTCA
GAGAAAGAAGAGACCCCACTCGGGCTGCAAAAGTGAAGACCAAGAGGTTTTCAGTGAAGTGAAG
GTGACAGTGTCTGCCGCTCTCAGCCCTCGCTGTCTCTCTCGCCGCTCTGCTGGGCTCCCACTTTGGCA
CCCTCAGCTTGGGGAGTTCGCGGGAGTGGGAGGAGGGCGGGCAGGAACCGGGCTCGCGCGACGCTTCGGGGCAG
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TAGCACTGGGGCAGCAGCTGTGTGCTCGATTCTCTGCTGGGCTTAGCTGCTTCCCCCGGGGAGGGCTCGG
GACCTCAGAGCTCTCATGCTGACCTCTCCCCACCCCGCTGGGCTCTGTGCGCGCGAGGCTCCCCAAGGAG
CGCGGCCCTCTCAGTCAAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGATGCGGGTGCACAGCGGGGA
CTGGCAGCGAGCTCCACTGCTCGCCAGTGTGGATCACTGGTGAAGCTCTGGCTCTGAGTCTGGTGG
GGACTTGGAGAACCTTTATGTTCTGACTAAGGATTGTAATACCAAGTGGGCACTCTGTATCTAGCTCAAGGT
TGTAAACAGCAATCAGCAACCTGTGTCTAGCTCAGTGTGTGATGATGCACTCAACACTGTATCTGGT
ACTCTGTGGGACTTGGAGACCTTTGTGTCCACTCTGTATCGACTAATCTAGTGGGATGTGGAGAACCT
TTGTGTCTAGCTCAGGATCGTAAACGCAACCAATCAGCACTCTGCAAAACAGGCACTTGACTCTCTGTAAAT
GGACCAATCAGCAGGATGTGGTGGGCGAGACAGAGATAAAGAGTGGCTGCTGAGCCAGCAGTGAACACCC
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FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862
><subunit 1 of 1, 571 aa, 1 stop
><MW: 62282, pI: 5.56, NX(S/T): 1
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IPFAQPPPLGPD RFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC
LVLNVYSPAIEVPAGSGRPFVMVWHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGF LDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPPVAAGLF
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVDGTVPFKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWLLDTMEQMSREDMLA
ISTPVLTSLDVPPPEMMPTVIDEYLGNSDAQAKQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPF LMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQQKQNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTCAG
TTTTGCTGTCTATAGTTCATGACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAA
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCT
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTG
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATC
TTTTGCAAGAAAAAATACGGAGTAACTTCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTTAGATTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT
TTTTGGAAGTATCTTGCAACCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG
AGGATCTATGAGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTG
GTCTCATTTTAAACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAATGTGGCA
ATGAAGGATTTTTTTTTTAAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCAGGATGAG
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACT
TCCTCTGACCATACTAAGAATTGAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACCTTT
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAAATGTAAATATATATACATAGATTCAAAATCCTTATATAT
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTCTTTTAAAGTACAGGTTCCCTAGTGTTTT
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TATAACATTTGAAAAGCTTCATCAAAAAAAAAAAAAA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL
EKYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVES
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLNVNPEGQVVKFWRPEEP
IEVIRPDIAALVRQVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

TGTCGCTTGGCCCTCGCCATGAGCAGACCCGCGAGCGTCCCCTCCCCCGCCGCCCTCTGCTTCTGCTGCTGCTA
 CTGGGGGGGCCCCACGGCTCTTTCTGAGGAGCGCCGCCCGCTTAGCGTGGCCCCAGGACTACCTGAACCA
 TATCCCGTGTTTTGGGCGAGCGGGCCCGGACGCTGACCCCGCAGAAAGGTGCTGACGACCTCAACATCCAGCGA
 GTCTTGGCGGTCAACAGGACGCTGTTCATTGGGGACAGGGACAACTCTACCGCGTGTAGACTGGAGCCCCACG
 TCCACGGAGTTCGGGTACACAGGAAAGCTGACCTGGAGATCTAAACCCAGCGACATAAACGTTGTGCGATGAAG
 GGCACAAACAGGAGGCGAGTGTGCAAACTTCGTAAGGTGCTGCTCTCTGGGACGAGTCCACGCTTTTGTGTG
 GGTTCCAAACGCTTCAACCCGGTGTGCGCAACTACAGCATAGACACCTGACGCCGTTCGGAGACAACTACAG
 GGTATGGCCGCTGCCGTAGCAGCCCAAGCACGCCAATGTTGCCCTCTTCTGACGGGATGCTCTTACAGCT
 ACTGTTACCGACTTCTAGCCATTGATGCTGTCTATCTACCGCAGCTCGGGGACAGGCCACCTCGGCACCGTG
 AAACATGACTCCAAAGTGTCAAGAGCCTTACTTTTGCCATCGGTGGATGGGCGAGCCATGTCTACTTCTTC
 TTCGGGAGATTCGATGGAGTTTAACTACCTGGAGAAGTGGTGGTGTCCCGCTGGCCCGAGTGTGCAAGAAC
 GACCTGGGAGGCTCCCCCGCTGCTGAGAAAGCAGTGGAGTCTTCTCTGAAGGCGGGCTCAACTGCTCTGTGA
 CCGCGAGACTCCCATTTCTACTTCAACGTCGTCAGGCTGTACGCGGCTGGTCAGCCTTCGGGGCGCGCCCGTG
 GTCTTGGCCGTTTTTTCACGCCCAACAGCATCCTGGCTCGGCTGTCTGCGCTTTGACCTGACACAGGTG
 GCAGCTGTGTTTGAAGCCCGCTTCGAGAGCAGAAGTCCCCGAGTTCATCTGGAGCGCGGTGCCGAGGATCAG
 GTGCTCGACCCGGCGCGGTGCTCGCAGACCCCGGGATGCAGTACAATGCTCCAGCGCTTGCCTGGATGAC
 ATCTCAACTTTTGTCAAGAACCACTCTGTATGGACGAGCGGTGCCCTCGCTGGCCATGCGCCTGGATCCTG
 CGGACCGCTGATGAGGACACAGCTGACTCGAGTGGCTGTGGAGCTGGGAGCGGCCCTGGGGCAACCAGACGCT
 GTCTTCTGGGTTTCTGAGCGGGGACGCTCTCAAGTTCTCTGTCGGCCCAATGCCACCACTCAGGACGCTGT
 GGGCTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGCCGAGCAGGTGTGACGCGCCCGCGGCTGGGCGAGCA
 GGGCAGCGGCTGTGAGCTTGGAGCTGGACGAGCTTCGGGGGCTGCTGGCTGCTTCCCGCTGCGGTGCTG
 CGAGTGCCTGTGGCTGCTGCCACAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGCT
 GGGTGGGCCCGCCAGGCTCTGCATCTTCTCAGCCCGGCGACAGAGCGCTTGTAGCAGGAGCTGTCCGG
 GCGACACCTCAGGCTTAGGGGATGCACAGGACTCTCTCGGGCCAGCCTCTCCGAGGACCGCGGGGCTGGTG
 TCGGTGAACCTGCTGTAACCTGCTCGTGGCGGCTTCTGTGGGAGCCGTGGTGTTCGGCTTCAAGCTGGG
 TGGTTCTGGGCTCTCGTGAGCGCGGAGCTGGCCCGCGCAAGGACAAGGAGCCATCTTGGCGCAGCGGGCG
 GCGAGGCGGTGCTGAGCTGAGCGCTGGGCGAGCGAGGCGCAGGGTCCCGGGGCGGGGCGGAGCGGT
 GGCCTGCGCGCGGGTTCCCCGGAGGCTGCTGCGGCCCTGATGCAGAACGCTGGGCCAAGGCCACGCT
 CTGAGGGGCGGCCCAACGACCTGAGCTCGGGCTGCTGCCACGCGCGAGCAGCGGCTGCCGAGAAGCG
 TCGCCTTATCTCTCTCTGCTGTGGGCGCGCGCGGCCCTTGGACCGAGCTCAGCGCGGATGGCTTCCCGG
 CCGCAGCGCGCTCTATGCTGCCCGCGCGCGCGCTCCACGCGGACTTCCGCTCAGCCCCCAGCGCAGC
 CGGACCGCGCGGGTGTGTCCGCGCCACGCGGCCCTTGGACCGAGCTCAGCGCGGATGGCTTCCCGG
 CCTGTGAGCGCGCGCGCGAGCGCTGAGGAGGCACTGGGCCCGCAGCGCTCTCGCGCGCCACCTCGCG
 CGCACCGACGTTCAACAGCGGTCGAGGCGCGGCTGGGGAACCGCACCGCGCTGAGGCTGGGAGGACAG
 GACTTGGCCACCTCTCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCTAGGCGCGGGGCCCCCG
 ATGCTTGGACACTGCCACCGACCGGAACAGGAGCGAGAGCGGTGCCAGAACTGGGGGCGGCGCAACTCG
 AGTGGGTGCTCAAGTCCCCCGCGGACCCCGCGGAGTGGGGGGCCCCCTCGGCCAAGGAAGCACAAACG
 CTGCGCTTCCCTTACCOCGGGCGAGGACGCTGAGACGTTTGGGGTGGTGGGCGGAGGACTTGTGATG
 GATTGAGGTGACCTTATGCGCGTAGGTTTGGTTTCTTTTTCAGTTTGGTTTCTTTGCGGTTTCTTAAC
 AATTGCAACTCCGTTCTCGGGTGGCGGAGGAGGCTTGGACGCGGTTGGGGAATGGGGGCGACAG
 CTGCAGACTAAGCGCTCCCCACCCCTGGAAAGTTCCTCCCCACCGAGCGGCTGGCGTGTGGGTGTGG
 TSGCTGTGCTGCTGCTTGTGTGCAAGGGGCGGGGAGGTGGCGTGTGTGCTGTCACGAGCGAGCTGTG
 TGGCGTGTGCTCACTGGGCGACGCTGCAGGGTGTGTGTCCAGAGCGAGCATGTGTTGGCCCGAGCGG
 TGGGCTTGGCTGAGCGAGCTGGGGCTTCCAGAAGCGCGGGGCTTCCGAGGTGGCGTTAGGATTGTGAAC
 CCGCCCCACTCTGAGAGGCAAGCGGGCAATGCGGGGTTTCAAGCGAGGACAGGAGGCGCTTGGCGGA
 AGTCACATCGGCAGCGTGTCTAAAGGGCTTGGGGCTTGGGGCGCGAGGTTGGTGGGCGCTCTGTAA
 ATACGGCCAGGGTGGTGAAGAGTCCATGCCACCGCTCCCTTGTGACTCCCCCTATGACTTCAAGCTGA
 CCGATGATGCCAGTGGCTGGCTGGTCTCTGCTCTTTGGAGTTTGCTCCCCAGCCCCCTCCCATCAAT
 AAAACTCTGTTTACAAACAAAAA

FIGURE 16

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145
><subunit 1 of 1, 888 aa, 1 stop
><MW: 95285, pI: 8.89, NX(S/T): 8
MQTPRASPPRPALLLLLLLGGAHGLFPPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGA
DDLNIQRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGQEG
ECRNFVVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNI SGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFREI
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSPVPGDSHFYFNVLQAVTG
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHA PWILRTLMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPRDRCGRPGGGETGQ
RLLSLELDAASGGLLAAFPRCVVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGCSCIFLSPG
TRAAFEQDVSGASTSGLDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGGGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLSGLLFTPEQTPLPQKRLLTPHPHPHALGPRAWDHGHPLLP
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTG
PLDPASAADGLPRPWSPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHLLPYGGADRTAPPVP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTTCATCATTGTCTTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC
AGAACGCCAGGGGACCTCACCTGGGCGCGCCGGGCACGGGCTTTGATTGTCTGGGGTCG
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG
CGATCGGCCGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC
ATTTATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCC
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTACATCTTCTCCAGGCGAAAAGGTCT
TCCAGGTGAAAGTCTCAGCACCAGAGGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGAC
CGAAAAGATGGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAATCTGAAGGT
GGAAATTAATTCGAAGGCCAACATGTGGCCAAATCCCCATATATTTTAAAGGGCCGGTTT
ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA
GATTGCAGTAGAAATCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTCGGT
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCACGTACGATTTGACTGATTCTGTCTGTG
GAAACCATGGGCCGGTAAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG
GGAAAGCAAAAATTCCTGCGCTCTGGAGAGGGCGAGACAGCCGCAAGAGAGACTCGAGC
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTACCAACTTTTTCTTC
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTCAATTTTTGATTCTT
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTGC
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCATCTACTATGAACATTTTACAATGAG
CTGCAGCCCTGGAAACACTACATTCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACT
TAAATGGCGGAAAGATCACGATGAAGAGGCCAAAAGATAGCAAAAGCAGGACAAGAATTTG
CAAGAAATAATCTCATGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACACAGAC
TGAGGACGACCTCTTCCCTGTACTTGCCATAGGAAAAAGACCAAAGATGAACCTCGATATG
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT
TTTTTAAGTATTAATTCATGGACAATATAAAATCTGTGTGATTGTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAGTACATTTTTAGAATTTTATAA
TAAACACCTTTATTTTAAAGGAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917
><subunit 1 of 1, 502 aa, 1 stop
><MW: 58043, pi: 7.94, NX(S/T): 2
MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVLPARYFYIQAVDTSGNKF
TSSPGKEVVFQVKVSAPEEQFTRVGVQVLDKDGFSFIVRYRMYASYKNLKV EIKFQGQHVAKS
FYILKGPVYHENCDCPLQDSA AAWLREMNC PETIAQIQRD LAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKRLELVKLSRKHP ELIDAAFTNFFFFKH DENLYGPIVKHISFFDFFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYE HFYNELQPWKHYIPVKS NLSDLLEKLKWKADHD EEA KK
IAKAGQEFARNNLMGDDIFCY YFKLFQ EYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA
GCCTAGCGTGTCCAC**GATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGGGCTCTTCTTCGGGGATTCTTCCCAGCTCCCGTTCGTTCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCGAACCTCGGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTTGTGGAA
AAAGGAGCATCTCACAGTTTGTGGGCTGAAGCAAAGCCACTACAGTTTACTATGCGCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGACGTCACTCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTTAAATTAATCCCAAAGCATTTTGTGGAATATGATGGAACAAC
CTCATTTTTTCGTGTGAGATTACACAGAGGTGGATAATAATGTACAGAGGCATTGTGGATAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTACGGGCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGC
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTACC**CA**ATTGTCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCAGCTCCA**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACC**GA**
TTCCAAAGACAGTGTAGGGAGCCTCCTATTTCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTTACATTTGAATACAGTGCGACTTAGTAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAAGATCTCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAAC
GGATCAGACTGTACTTGGAGGAAAAGCATTAGAAGTCTTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCTGCTCTGCTCAGCGTCCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAAGT
CCCAGTGTCATCTCCTGGGTTTTCTCTGCTCTTTATTTGGTGATCTGCTGTTCTTCGCGCG
TTCACGTCAATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGGCTCTCGTGGCTG
GCGGAGGCTGCCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGGCTCTGGG
TGTCCCAGACAGGTGTTACATCTGTGCTGTCAGGTGAGTGCCTCAGTTCTTGAAAGCT
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCC
CCCAGCTGAGGGGGTGTGTAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGTCAAAAGGAGACTTGTGCGCACCCAC
TCATCTGCCACCCCAAGAATGCATCTGCCTCATCAGGTCCAGATTTCTTTCCAAGCGGA
CGTTTTCTGTTGGAATTTCTAGTCTTGGCCTCGGACACCTTCAATCGTTAGCTGGGGAGTG
GTGGTGAGGCAGTAGAAGAAGGCGGATGGTACACTCAGATCCACAGAGCCACAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCACCCCAACCTGCACAGCCCTCATC
CCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCAGACACTCAGCTT
TGTCTACAGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCAGGCTTGCACTTCCGCGC
CCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920
><subunit 1 of 1, 310 aa, 1 stop
><MW: 33875, pI: 7.08, NX(S/T): 2
MRLGSGTFATCCVAIEVLGIADVFLRGFFPAPVRSSARAEGHAEPPEPSAGASSNWTTLPP
PLFSKVIVILIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPHFVEYDGTTSFFVS
DYTEVDNNVTRHLDKVLKRGDWDILHLHYLGLDHHIGHISGPNSPILIGQKLEMSDVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAAT
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATG
AAGTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACA**ACT**GAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCAGAGTCCAGTGTACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGCG
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACCTCATTTCTGTCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR
PSCTEGTTSPWTAIDLQGSCEGYLCNRKSMTPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCACGCGTCCGGGACAGATGAACCTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG
 GAAAGGACAAAAAGACCCCTGGGCTACACGCGCTAGGTCAGGGTTTCTACTGCTGTTCT
 TTTATGCTGGGAGCTGTGGCTGTAAACCACTAGGAAATAACGTATGCAGCAGCTATGGCTGT
 CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCTCTGTTTCTTTTCTTTTGGGGAGGTG
 CTTTGGCAGGTTCTGGTTTGGACGTTTATTCGGTGACTGAGGAAACAGAGAAGGATCCCTT
 TGTGCTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCA
 GGTGGTTTCCGATGATAACAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA
 CAAATGAGAAACTGGACCGAGGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTC
 CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
 TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATACAGAAATACAGCTG
 AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACATTAACCGGTATCCAA
 AACTATACGATCAGCCCAACTCTTTTTCATATTAACATTAGTGGCGGTGATGAAGGCAT
 GATATATCCAGAGCTAGTGTTTGGACAAAGCACTGGATCCGGGAGGAGCAGGAGCTCAGCT
 TAACCCCTCACAGCGCTGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC
 GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTCCCCAGGCTCTGTATGAGACCCAGGC
 TCCAGAAACAGCCCCATTTGGGTCTTTATTTGTTAAGGTATGGGAGAAGATGTAGACTCTG
 GAGTCAACGCGGAAGTATCCTATTCTTTTGTATGCTCAGAAAAATATTCGAACGACCTTT
 CAAATCAATCCTTTTCTGGGGAAATCTTCTCAGAGAATTGCTTGTATTAGTTAGTTAGTAA
 TTCTTACAAAATAAATATACAGGCATGACCGGTGGAGGCCCTTCTGCAAGATGAGGGTTT
 TAGTGGAAGTATTGGACCAACATGACAATCCCCCTGAACTGATCATCATTTTCCAAC
 TCTGTTGCTGAGAATTTCTCTGAGACGCCGTGGCTGTTTAAAGATTATGACAGAGACTG
 TGGAGAAAATGGAAAGATGTTTGTACATTCAAGAGAATCTGCCATTCTCTACTAAAACCTT
 CTGTGGAGAAATTTTACATCCTAATTACAGAAGCGCGCTGGACAGAGAGATCAGAGCCGAG
 TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAACCCGAGCAACAAT
 AACGGTCTCTGGTCTCCGACGTCAATGACAACGCCGCCGCCCTTACCCAAACCTCTACACCC
 TGTTGCTGCGGAGAACCAACAGCCCCGCCCTGCACATCGGACGCTCAGCGCCACAGACAGA
 GACTCGGGCACCAACGCCCAAGGTCACTTACTCTGCTGCGCGCCCAAGACCCGCACCTGCC
 CCTCGCCTCCCTGGTCTCCATCAACGCGGACCAACGCCACCTGTTGCGCCTCAGGCTCGCTGG
 ACTACGAGGCCCTCGACGGCTTTCGAGTTTCCGCTGCGCGCCACAGACCGCGGCTCCCCCGG
 CTGAGCAGAGAGGCGCTGGTGCCTGCTGGTGTGAGCGCCAACGACAATCGCCCTTCGT
 GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGCCGAGC
 CGGGCTACCTGTTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACCGCTGCTG
 TCGTACCAGTGTCAAGGCCACGAGGCCCGGGCTGTTCCGGTGTGGGGCGCACAGTGGGGA
 GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAAGCAAGGCTCGTGGTGGCTTG
 TCAAGGACAATGGCGAGGCTCCTCGCTCGGCCACCGCCACGCTGCATTGCTCCTGGTGGAC
 GGCTCTCCCGACCTACTCTGCTCTCCCGGAGGCGGCCCGGCCAGGCCCCAGCCCGAGGC
 GCACTTGTCTACCGTCTCACTGGTGGTGGCGCTTGCCCTCGGTGCTTCGCTCTTCTCTCT
 CGGTGCTCCTGTTCTGTGCGGTGCGGCTGTGACGAGGAGCAGGGCGGCCCTCGGTGGGTGCG
 TGCTCGGTGCCCCGAGGTTCTTTCCAGGGCATCTGGTGGACCTGAGGGCGCTGAGACCCCT
 GTPCCAGAGCTACCAATGAGGTGTGTCTGACGGGAGGCCCGGGACAGTGAAGTTCAAGT
 TCTTGAACACAGTTATTTTCGATATTACGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAAT
 TCCACTTCCGAAATAGCTTTGGATTAAATATTCACTAAAGATCTGTTTATGTTTCTATATAC
 TTTTGGTGTGTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT
 TATGCAACTCAAGCATATTTTCAAGTAGTATACCCCTGTGGTTTTACAATGTTTCATCAT
 TTTTTGCACTTAATAACAACTGGGTTTAATTTAATGAGTATTTTTTCTAATGATAGTGT
 AAGGTTTTAATCTTTCCAACCTGCCAAGGAATTAATTACTATTATCTCATTTACAGAAAT
 CTGAGGTTTTGATTCACTTTCAGAGCTTGCATCTCATGATCTTAATCACTCTGCTCATATG
 TACTTCTCTATTAAAGAAAGGCATATCTACATTTCCAACTCATCTTAACATTTCTATATATT
 CGTGTTTTGAAACCATGTCTATTTTCTACATCATGTATTTAAAAAGAAATTTTCTCTAC
 TACTATGCTCATGACAAATAAACAAGCATATTGTGAGCAATCTGAACATCAATAATAC
 CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGGCCAAATATTTT
 CTTATGTTAACTTTTGTGATGTATAAAACAGACTATGCCTTATAATTGAATAAAATTTATA
 ATCTGCTGGAATTAATAAAATAAAACATTTTGAATGTGAAAAAATAAAAAAATAAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFFPRQRQVLFLEFLFWGVSLAGSGFGGRYSVTEETEKGSFVVNLAKDLGLAEGELAAAR
GTRVVSDDNKQYLLLDSTHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDPPFQIYRAELVRV
DINHAPVFQDKETVLKISENTAEGTAFRLERAQDDPGGLNGIQNYTISPNSFFHINISGGD
EGMIYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYE
TQAPENSPIGFLIVKVAEDVDGSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQAODGGGLSARCVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGENGMVCYIQENLPFLKPSVENFYILITEGALDREIRAENYITITVTDLTGTPRLKTE
HNITVLVSDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTSYLLPPQDP
HLPLASLVSINADNGHLFALRSLDYEALQAFEFVRVGTDRGSPALSREALVRVLVDANDNS
PFVLYPLONGSAPCTELVPRAAEPGYLVTKVAVDGDGSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDFGFSQPYLPLPEAAPAAQAO
AEADLLTVYLVVALASVSSLELLSVLLFVAVRLCRRSRAASVGRCSVPEGFFPGHLLVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIO

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234
><subunit 1 of 1, 507 aa, 1 stop
><MW: 56692, pI: 5.22, NX(S/T): 3
MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVQYIDLHQDEFVQTLKEWVAIESD
SVQVPVPRFQELFRMMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTK
GTVCYFGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYP SL SIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTPIAKMFQEIVHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
A AFFLEMAQLH

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTAAAGGTTGCCGCTAGCCGCTGGGAATTTAAGGGACCCACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTGTCTATGGGACCTGTGCGGTT
GGGAATATTGCTTTTCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTTGCCCGAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAACCTGAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGAGAAGGG
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCAGCGTGGAGGTCACAT
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCAGCTGC
TGAAACTGCATGTCTACAGGAACTTGGAAGGAGATCACAGATGGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGGAAGGGAAGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCAACTTGACCGAGAAGATCTTTTGACCCTTGCCCTTGAG
CCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCTGCACTCTCCCTGCTCCACAG
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAAGCTTGAGCTGTTCTCTCCATCTAACC
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGTGGGGTGGAGG
TCCTGCTCCTAGAGATGAAGCTATCCAGCCCTTAATGGCAGGTGATGTGCTGACAGTA
CTGAAAGCTTTCCTCTTTAACTGATCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGTCTGTTTTTAGACCTTCCAAGGAAGA
GGCCAGAACGGACATTCTCTGCATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCTGGAGTGTCTGATAATTTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCACCATATAGTTTTATAGGT
GCTCAACTTCTATATCGCTATTAACTTTTTTCTTTTTTCTA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSR TGRSREVL
ELGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLYAKQSQTMTLK
GLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG
HVLPAETAACLQETWTGKEITDGEEKTEGEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL
```

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCCATGGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCTGGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTGAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCACCGGCACACAGTGGCTTCCATCGCTACCAAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAACTCGAGGCTCTTGGAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGATTAGCTGCGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274
><subunit 1 of 1, 223 aa, 1 stop
><MW: 25402, pI: 8.14, NX(S/T): 1
MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFPYELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAPRQRFWRHWLVTDIKGADLK
KGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTTCAGTCCCCTGGACTGTAGATAAAGA
CCCTTTCTTGCCAGGTGCTGAGACAACCACACTATATGAGAGGCACCTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTGGGAATCCAGAATCCAGAAATGTGTTTG
TATTGTGAGAAGGTTGGAGAACAGCCACATTGCAGCTAAAGAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAAACCCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCGCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA
CTGA¹ACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGCTTAAAGTTTCTGGTTCCCAATGTGT
TTTCGTCTACATTTTCTTAGTGTCAATTTACGCTGGTGTGAGACAGGAGCAAGGCTGTG
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCTCTCAAGCTGGTGTGTGTAG
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACTGAGCTTTCTTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTTCTGTTTGTCTTATTCCTCTTGGGATGATATCATCCAGTCTTTAT
ATGTTGCCAATATACCTCATTGTGTGAATAGAACCTTCTTAGCATTAAGACCTTGTAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTGTCTTATTCCTCTTGGGATGATATCA
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGAATAGAACCTTCTTAGCATTAAG
ACCTTGTAACA²AAAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCTAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAAC³TGATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTFGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIQNPENCLYCEKVGEP
PTLQLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIIL
TSELGKSYNTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACCATGAGGACGCGCTGGGCCTCTGCCCGTGCTGCTGCTG
CTCCTGGCGGGAGCCCCGCGCGGGCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTCGCCCCCGTGTGGAAAGTGGCCCAGGTAGATTTCCTTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTGGTATTCCTGTTGG
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAATAAAGTTATGTGAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGAAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA
GTTAGCAACCATGCTTCTCATTCCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC
ATGTTGATTTGGTCACTAAAAAGAAGAAAGGACTAACAAGCTTCACTTTTATGAACAATA
TTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTAATGGAGTAATGGTACTTTTA
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTCTAACAC
AGACTTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTACG
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAATCAAATAAAGAAATCTCTTC
ACATGGA

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011
><subunit 1 of 1, 136 aa, 1 stop
><MW: 15577, pI: 8.88, NX(S/T): 0
MRTPGPLPVLLLLLAGAFAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNYCVLDKLRDEVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNAL EYP
IPVTTVL PDRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGCGGACAGCGCTCCCTCTACCTGGAGA
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA
GCCGCCAGTCCCGGCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCTGTTTTTAC
TCCTCCTTTTCATTACATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA
AGCCGAGCGTGGAAGAAATGCGGGTTCCTCGGGACCGGCACCTTGGATTCTGGTGTTAGTGCTCC
CGATTCAAGCTTTCCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA
AGTGCGAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAATAAAC
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTGTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA
TATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTTAACCCTGGAAGACATTGTCCATAAAATCGCTGCCAGGATTAT
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCCTTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAATTAATCT
CAAAGGAAGCCAACAATTTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGG
AGAAAACGATGAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAAGGAGAACTA
AAACCTACAGTGAAGACAACTTTGAGGAACCTCCAATATTTCCCAAATTTCTATGCGCTACTG
AAAAGTATTGATTGAGAAAAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAAC
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTT
CCTACCTTGAAAACCTTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAT
GCTACTGACAAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAGAAGGAATATGGAAGCTTGAAGGATTCACAA
AAGATGATAACTCCAACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAAAGCCTAT
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGA
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAAACAAGCTGATGCTTATGTGGAGA
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAACACTTC
TAATTCTGTGATTAATAATTTTTGACCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT
TAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDET
VSNLTILTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

[illegible][illegible]

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTAERALRENERHAFTCRVAGGPGT
PR
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLD
AQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSSASLPAPGSPSRHPSLISSDSNNLKLNNVRLP
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY
RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCTGGGCCCGAGGGGCTGGAGCCGGGCCGGGGCG**ATGT**GGAGCGC
GGGCCCGGGCGGGGCTGCCTGGCCGGTGTCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGTGAAGCTGCTC
AATACGCACCACCGCTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGCGCTAGAGGCGTCTGGACGACGCCAATAGTACTGGCGGATCCGCGGGC
GCTCGGAGGGCGGGTGCCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG
TTCCTGTCAGTACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG
CATGCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTACGATGAACTC**TGAG**TGTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGCTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTC
AAGTGCCTTTGTGATTAAGAATGTTGGTCTATGAAA

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVESDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL
SNNQEVSAFGEDGEGDDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTGGAAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAACTTCATCTTCTTGGATGAGATGAACACTTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAAACTTACACA
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT
CGTCATC**ATGT**CTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTGGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC
AACATGGGCGATAGGACTAGCATGGTGCAGGACCTGGCTCTCAAGCTCCACATCCTGGAT
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG
GGTGTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCTTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTTCT**TAA**CATCTCAGATGAAACCAAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAAGTGGGAAT
CTGAGTTTGACCTAAAAGTCATTAAATAACATGAATCCCATTAAAAAAAAAAAAA

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

.><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDFGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTTCTCAGGACCCTCGCCATGAAAG
CCCTTATGCTGCTCACCCCTGTCTGTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTAC
TCCTGCTACAAGGTCCCCTGTGCTGGGCTGTGTGGACCGGCAGTCTCGCCGCCTGGAGCCAGG
ACAGCAATGCCTGACAAACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCACTCC
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAG
ACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTTCCACCTCACACCCCTTCACTCTCCTTTTTCTGGGT
CCCTTCCCACTTCCCTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT
ATACTCTGCTGTCCCTTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGCTTCTGTG
TTGTCCCCAGTGAAGGCTCCCAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCAGGCTCCCATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAA
TGTCTGAGCTGGAAAAAAAAAAAAAAAAAAAA

FIGURE 44

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN
LRCGTPEEPCQEA FNQTNRKLG LTYNTTCENKDNCNSAGPRPTPALGLVFLTSLAGLG LWLLH
```

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA
GTCGGGCCGTTCTTCGCCCGCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGCTCGCGCGCGCT
ACCGCACCCAGGTTTCGGCCGTAGGCGTCTGGCAGCCCCGGCGCATCTTCATCGAGCGCAT
GCGCGAGCCTGCGGGCCGGAGCGCGCGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTTACCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCAAAAGTCATACAGTGTC
AGAACAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCCTCTGAAGACAGTATGT
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCTTCGAGAAAC
TGAAGGAGTCTGGAAGCAGCACGGCTTTGCCCTCTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAAGCTATAAGCTGTTCTCGAGTGACGGGCAGTATTCTCC¹TCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAAGATTCACCAACTCAGCAGGACCTCCTCCCCAGGCTTT
AAGTCTGAGTTACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGCGAGTGC
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTCTGAGCAGGCTTGGGAATG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCCTACCTGGCACGTGGAATAGGGCTTACTACCCCTTCA
TGGAGGCTCGGGCAGCTATTCTGGTATGTTCAAACCTCAGACACGAAAACGAACTGCATCAG
GATATGGTGGTACCAGGAGACGAT²AAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTCATCACTTCTCTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAAG
GGGATATTCAAAAGTCTGTGGTGTATGTCCAGTGATGCTTTTGTATTCTATTATTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAAACATGCAGATGTA
TATTGCAGTTTTTGAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAAAC
CTGTGATGCCCTAAGAAGCATTAAAGATGAAGGTGTTGTACTAATAGAAACTAAGTACAGAA
AATTTCAAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTGATGTTTGTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGTGGAAAATAAGCATCTA
GAAGGTTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTCGT
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGCTTTTAATAACAAAAGCATGCAGTTCT
TCTGTGAAATCTCAAATATTGTTGAATAGTCTGTTTCAATCTTAAAAAGAAATCA

FIGURE 46

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPI
QLKCVGGTAGCDSYTPKVIQCQNKGWGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSSEDQY
VLRGSCGLEYNLDYTELGLOKLKESGKQHGFAFSFDYIYKWSADSCNMGLITIVVLLGIA
FVYVKLFSLSDGQYSPPPYSEYPPFSHRYQRFNSAGPPPPGFKSEFTGPQNTGHGATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYPPSYPPSYPGTWNRAYSPL
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318